

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Lester, Henry A., et al.

(ii) TITLE OF INVENTION: DNA ENCODING INWARD RECTIFIER, G-PROTEIN
ACTIVATED, MAMMALIAN, POTASSIUM KGA CHANNEL

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Cooper & Dunham
- (B) STREET: 30 Rockefeller Plaza
- (C) CITY: New York
- (D) STATE: New York
- (E) COUNTRY: USA
- (F) ZIP: 10112

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US Not Yet Known
- (B) FILING DATE:
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: White, John P.
- (B) REGISTRATION NUMBER: 28,678
- (C) REFERENCE/DOCKET NUMBER: 43717/JPW/TEP

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 977-9550
- (B) TELEFAX: (212) 664-0525
- (C) TELEX: 422523 COOP UI

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 32..1534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA	52
Met Ser Ala Leu Arg Arg Lys	
1 5	
TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC	100
Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly	
10 15 20	
TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC	148
Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro	
25 30 35	
AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG	196
Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val	
40 45 50 55	
CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC	244
Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu	
60 65 70	
TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC	292
Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe	
75 80 85	

ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG	340
Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp	
90 95 100	
GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC	388
Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn	
105 110 115	
TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT	436
Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu	
120 125 130 135	
TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC	484
Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile	
140 145 150	
ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC	532
Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile	
155 160 165	
CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG	580
Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys	
170 175 180	
ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT	628
Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His	
185 190 195	
GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG	676
Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val	
200 205 210 215	
GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG	724
Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys	
220 225 230	
CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC	772
Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp	
235 240 245	
CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT	820

Gln	Leu	Glu	Leu	Asp	Val	Gly	Phe	Ser	Thr	Gly	Ala	Asp	Gln	Leu	Phe		
	250						255					260					
CTT	GTG	TCC	CCT	CTC	ACC	ATT	TGC	CAC	GTG	ATC	GAT	GCC	AAA	AGC	CCC	868	
Leu	Val	Ser	Pro	Leu	Thr	Ile	Cys	His	Val	Ile	Asp	Ala	Lys	Ser	Pro		
	265					270				275							
TTT	TAT	GAC	CTA	TCC	CAG	CGA	AGC	ATG	CAA	ACT	GAA	CAG	TTC	GAG	GTG	916	
Phe	Tyr	Asp	Leu	Ser	Gln	Arg	Ser	Met	Gln	Thr	Glu	Gln	Phe	Glu	Val		
280					285				290					295			
GTC	GTC	ATC	CTG	GAA	GGC	ATC	GTG	GAA	ACC	ACA	GGG	ATG	ACT	TGT	CAA	964	
Val	Val	Ile	Leu	Glu	Gly	Ile	Val	Glu	Thr	Thr	Gly	Met	Thr	Cys	Gln		
			300					305						310			
GCT	CGA	ACA	TCA	TAC	ACC	GAA	GAT	GAA	GTT	CTT	TGG	GGT	CAT	CGT	TTT	1012	
Ala	Arg	Thr	Ser	Tyr	Thr	Glu	Asp	Glu	Val	Leu	Trp	Gly	His	Arg	Phe		
			315					320					325				
TTC	CCT	GTA	ATT	TCT	TTA	GAA	GAA	GGA	TTC	TTT	AAA	GTC	GAT	TAC	TCC	1060	
Phe	Pro	Val	Ile	Ser	Leu	Glu	Glu	Gly	Phe	Phe	Lys	Val	Asp	Tyr	Ser		
	330					335					340						
CAG	TTC	CAT	GCA	ACC	TTT	GAA	GTC	CCC	ACC	CCT	CCG	TAC	AGT	GTG	AAA	1108	
Gln	Phe	His	Ala	Thr	Phe	Glu	Val	Pro	Thr	Pro	Pro	Tyr	Ser	Val	Lys		
	345					350				355							
GAG	CAG	GAA	GAA	ATG	CTT	CTC	ATG	TCT	TCC	CCT	TTA	ATA	GCA	CCA	GCC	1156	
Glu	Gln	Glu	Glu	Met	Leu	Leu	Met	Ser	Ser	Pro	Leu	Ile	Ala	Pro	Ala		
360					365					370				375			
ATA	ACC	AAC	AGC	AAA	GAA	AGA	CAC	AAT	TCT	GTG	GAG	TGC	TTA	GAT	GGA	1204	
Ile	Thr	Asn	Ser	Lys	Glu	Arg	His	Asn	Ser	Val	Glu	Cys	Leu	Asp	Gly		
			380					385					390				
CTA	GAT	GAC	ATT	AGC	ACA	AAA	CTT	CCA	TCG	AAG	CTG	CAG	AAA	ATT	ACG	1252	
Leu	Asp	Asp	Ile	Ser	Thr	Lys	Leu	Pro	Ser	Lys	Leu	Gln	Lys	Ile	Thr		
			395					400					405				
GGG	AGA	GAA	GAC	TTT	CCC	AAA	AAA	CTC	CTG	AGG	ATG	AGT	TCT	ACA	ACT	1300	
Gly	Arg	Glu	Asp	Phe	Pro	Lys	Lys	Leu	Leu	Arg	Met	Ser	Ser	Thr	Thr		

410	415	420	
TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA			1348
Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg			
425	430	435	
ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC			1396
Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr			
440	445	450	455
ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA			1444
Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro			
	460	465	470
CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT			1492
Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn			
	475	480	485
CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA			1534
Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr			
	490	495	500
TAGCAAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTGTAGT CCAATATTTG			1594
GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCAT			1654
CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA			1714
TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT			1774
TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA TATTCTGGAA			1834
AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA ATATATGTAT			1894
TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG CATAACATACA			1954
TACATGCATA TGCACAGACA CATAACACACA CATACTCATA TATATAAAAC ATACCCATAC			2014
AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCAA AAAAAAAAAA AAAAAACTCG			2074
AG			2076

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ala	Leu	Arg	Arg	Lys	Phe	Gly	Asp	Asp	Tyr	Gln	Val	Val	Thr	1	5	10	15
Thr	Ser	Ser	Ser	Gly	Ser	Gly	Leu	Gln	Pro	Gln	Gly	Pro	Gly	Gln	Gly	20	25	30	
Pro	Gln	Gln	Gln	Leu	Val	Pro	Lys	Lys	Lys	Arg	Gln	Arg	Phe	Val	Asp	35	40	45	
Lys	Asn	Gly	Arg	Cys	Asn	Val	Gln	His	Gly	Asn	Leu	Gly	Ser	Glu	Thr	50	55	60	
Ser	Arg	Tyr	Leu	Ser	Asp	Leu	Phe	Thr	Thr	Leu	Val	Asp	Leu	Lys	Trp	65	70	75	80
Arg	Trp	Asn	Leu	Phe	Ile	Phe	Ile	Leu	Thr	Tyr	Thr	Val	Ala	Trp	Leu	85	90	95	
Phe	Met	Ala	Ser	Met	Trp	Trp	Val	Ile	Ala	Tyr	Thr	Arg	Gly	Asp	Leu	100	105	110	
Asn	Lys	Ala	His	Val	Gly	Asn	Tyr	Thr	Pro	Cys	Val	Ala	Asn	Val	Tyr	115	120	125	
Asn	Phe	Pro	Ser	Ala	Phe	Leu	Phe	Phe	Ile	Glu	Thr	Glu	Ala	Thr	Ile	130	135	140	
Gly	Tyr	Gly	Tyr	Arg	Tyr	Ile	Thr	Asp	Lys	Cys	Pro	Glu	Gly	Ile	Ile	145	150	155	160

Leu Phe Leu Phe Gln Ser Ile Leu Gly Ser Ile Val Asp Ala Phe Leu
165 170 175

Ile Gly Cys Met Phe Ile Lys Met Ser Gln Pro Lys Lys Arg Ala Glu
180 185 190

Thr Leu Met Phe Ser Glu His Ala Val Ile Ser Met Arg Asp Gly Lys
195 200 205

Leu Thr Leu Met Phe Arg Val Gly Asn Leu Arg Asn Ser His Met Val
210 215 220

Ser Ala Gln Ile Arg Cys Lys Leu Leu Lys Ser Arg Gln Thr Pro Glu
225 230 235 240

Gly Glu Phe Leu Pro Leu Asp Gln Leu Glu Leu Asp Val Gly Phe Ser
245 250 255

Thr Gly Ala Asp Gln Leu Phe Leu Val Ser Pro Leu Thr Ile Cys His
260 265 270

Val Ile Asp Ala Lys Ser Pro Phe Tyr Asp Leu Ser Gln Arg Ser Met
275 280 285

Gln Thr Glu Gln Phe Glu Val Val Val Ile Leu Glu Gly Ile Val Glu
290 295 300

Thr Thr Gly Met Thr Cys Gln Ala Arg Thr Ser Tyr Thr Glu Asp Glu
305 310 315 320

Val Leu Trp Gly His Arg Phe Phe Pro Val Ile Ser Leu Glu Glu Gly
325 330 335

Phe Phe Lys Val Asp Tyr Ser Gln Phe His Ala Thr Phe Glu Val Pro
340 345 350

Thr Pro Pro Tyr Ser Val Lys Glu Gln Glu Glu Met Leu Leu Met Ser
355 360 365

Ser Pro Leu Ile Ala Pro Ala Ile Thr Asn Ser Lys Glu Arg His Asn
370 375 380

Ser Val Glu Cys Leu Asp Gly Leu Asp Asp Ile Ser Thr Lys Leu Pro
385 390 395 400

Ser Lys Leu Gln Lys Ile Thr Gly Arg Glu Asp Phe Pro Lys Lys Leu
405 410 415

Leu Arg Met Ser Ser Thr Thr Ser Glu Lys Ala Tyr Ser Leu Gly Asp
420 425 430

Leu Pro Met Lys Leu Gln Arg Ile Ser Ser Val Pro Gly Asn Ser Glu
435
440 445

Glu Lys Leu Val Ser Lys Thr Thr Lys Met Leu Ser Asp Pro Met Ser
450 455 460

Gln Ser Val Ala Asp Leu Pro Pro Lys Leu Gln Lys Met Ala Gly Gly
465 470 475 480

Pro Thr Arg Met Glu Gly Asn Leu Pro Ala Lys Leu Arg Lys Met Asn
485 490 495

Ser Asp Arg Phe Thr
500